

Amendments to the Specification

Please replace the paragraph beginning at page 42, line 5-28 with the following:

The variable segments of antibodies produced as described *supra* (e.g., the heavy and light chain variable regions of chimeric, humanized, or human antibodies) are typically linked to at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. Human constant region DNA sequences can be isolated in accordance with well known procedures from a variety of human cells, but preferably immortalized B cells (see Kabat *et al.*, *supra*, and Liu *et al.*, ~~W087/02671~~ WO 87/02671) (each of which is incorporated by reference in its entirety for all purposes). Ordinarily, the antibody will contain both light chain and heavy chain constant regions. The heavy chain constant region usually includes CH1, hinge, CH2, CH3, and CH4 regions. The antibodies described herein include antibodies having all types of constant regions, including IgM, IgG, IgD, IgA and IgE, and any isotype, including IgG1, IgG2, IgG3 and IgG4. The choice of constant region depends, in part, whether antibody-dependent complement and/or cellular mediated toxicity is desired. For example, isotopes IgG1 and IgG3 have complement activity and isotopes IgG2 and IgG4 do not. When it is desired that the antibody (e.g., humanized antibody) exhibit cytotoxic activity, the constant domain is usually a complement fixing constant domain and the class is typically IgG1. When such cytotoxic activity is not desirable, the constant domain may be of the IgG2 class. Choice of isotype can also affect passage of antibody into the brain. Human isotype IgG1 is preferred. Light chain constant regions can be lambda or kappa. The humanized antibody may comprise sequences from more than one class or isotype. Antibodies can be expressed as tetramers containing two light and two heavy chains, as separate heavy chains, light chains, as Fab, Fab' F(ab')₂, and Fv, or as single chain antibodies in which heavy and light chain variable domains are linked through a spacer.

Please replace the header beginning at page 108, line 2 with the following header:

D. Measurement of A β Levels

Please replace the table beginning at page 86 through page 89 with the following table:

Table 13: Key to Kabat Numbering for Light Chain

<u>KAB#</u>	<u>#</u>	<u>TYPE</u>	<u>mouse</u> <u>3D6 VL</u> (aa 1-112 SEQ ID NO:2)	<u>HUM</u> <u>3D6VL</u> (aa 1-112 SEQ ID NO:5)	<u>KABID</u> <u>019230</u> (aa 1-112 SEQ ID NO:6)	<u>A19-</u> <u>Germ-</u> <u>line</u> (SEQ ID NO:7)	<u>Comment</u>
1	1	FR1	Y	Y	D	D	Rare mouse, may contact CDR
2	2		V	V	I	I	Canonical/CDR contact
3	3		V	V	V	V	
4	4		M	M	M	M	
5	5		T	T	T	T	
6	6		Q	Q	Q	Q	
7	7		T	S	S	S	
8	8		P	P	P	P	
9	9		L	L	L	L	
10	10		T	S	S	S	
11	11		L	L	L	L	
12	12		S	P	P	P	
13	13		V	V	V	V	
14	14		T	T	T	T	
15	15		I	P	P	P	
16	16		G	G	G	G	
17	17		Q	E	E	E	
18	18		P	P	P	P	
19	19		A	A	A	A	
20	20		S	S	S	S	
21	21		I	I	I	I	

22	22		S	S	S	S	
23	23		C	C	C	C	
24	24	CDR1	K	K	R	R	
25	25		S	S	S	S	
26	26		S	S	S	S	
27	27		Q	Q	Q	Q	
27A	28		S	S	S	S	
27B	29		L	L	L	L	
27C	30		L	L	L	L	
27D	31		D	D	H	H	
27E	32		S	S	S	S	
28	33		D	D	N	N	
29	34		G	G	G	G	
30	35		K	K	Y	Y	
31	36		T	T	N	N	
32	37		Y	Y	Y	Y	
33	38		L	L	L	L	
34	39		N	N	D	D	
35	40	FR2	W	W	W	W	
36	41		L	L	Y	Y	Packing residue
37	42		L	L	L	L	
38	43		Q	Q	Q	Q	
39	44		R	K	K	K	
40	45		P	P	P	P	
41	46		G	G	G	G	
42	47		Q	Q	Q	Q	
43	48		S	S	S	S	
44	49		P	P	P	P	
45	50		K	Q	Q	Q	
46	51		R	R	L	L	Packing residue
47	52		L	L	L	L	
48	53		I	I	I	I	
49	54		Y	Y	Y	Y	
50	55	CDR2	L	L	L	L	
51	56		V	V	G	G	
52	57		S	S	S	S	
53	58		K	K	N	N	
54	59		L	L	R	R	
55	60		D	D	A	A	

56	61		S	S	S	S
57	62	FR3	G	G	G	G
58	63		V	V	V	V
59	64		P	P	P	P
60	65		D	D	D	D
61	66		R	R	R	R
62	67		F	F	F	F
63	68		T	S	S	S
64	69		G	G	G	G
65	70		S	S	S	S
66	71		G	G	G	G
67	72		S	S	S	S
68	73		G	G	G	G
69	74		T	T	T	T
70	75		D	D	D	D
71	76		F	F	F	F
72	77		T	T	T	T
73	78		L	L	L	L
74	79		K	K	K	K
75	80		I	I	I	I
76	81		S	S	S	S
77	82		R	R	R	R
78	83		I	V	V	V
79	84		E	E	E	E
80	85		A	A	A	A
81	86		E	E	E	E
82	87		D	D	D	D
83	88		L	V	V	V
84	89		G	G	G	G
85	90		L	V	V	V
86	91		Y	Y	Y	Y
87	92		Y	Y	Y	Y
88	93		C	C	C	C
89	94	CDR3	W	W	M	M
90	95		Q	Q	Q	Q
91	96		G	G	A	A
92	97		T	T	L	L
93	98		H	H	Q	Q
94	99		F	F	T	T
95	100		P	P	P	P

96	101		R	R	R
97	102		T	T	T
98	103	FR4	F	F	F
99	104		G	G	G
100	105		G	Q	Q
101	106		G	G	G
102	107		T	T	T
103	108		K	K	K
104	109		L	V	V
105	110		E	E	E
106	111		I	I	I
106A	112		K	K	K

Please replace the table beginning at page 90 through page 93 with the following table:

Table 14. Key to Kabat Numbering for Heavy Chain

<u>KAB#</u>	<u>#</u>	<u>TYPE</u>	<u>Mouse</u>	<u>HUM</u>	<u>KABID</u>	<u>VH3-23</u>	<u>Comment</u>
			<u>3D6 VH</u> (aa 1-119 SEQ ID NO:4)	<u>3D6 VH</u> (aa 1-119 SEQ ID NO:8)	<u>045919</u> (SEQ ID NO:9)	<u>Germ-</u> <u>line</u> (SEQ ID NO:10)	
1	1	FR1	E	E	E	E	
2	2		V	V	V	V	
3	3		K	Q	Q	Q	
4	4		L	L	L	L	
5	5		V	L	L	L	
6	6		E	E	E	E	
7	7		S	S	S	S	
8	8		G	G	G	G	
9	9		G	G	G	G	
10	10		G	G	G	G	
11	11		L	L	L	L	
12	12		V	V	V	V	
13	13		K	Q	Q	Q	
14	14		P	P	P	P	
15	15		G	G	G	G	
16	16		A	G	G	G	

17	17		S	S	S	S	
18	18		L	L	L	L	
19	19		K	R	R	R	
20	20		L	L	L	L	
21	21		S	S	S	S	
22	22		C	C	C	C	
23	23		A	A	A	A	
24	24		A	A	A	A	
25	25		S	S	S	S	
26	26		G	G	G	G	
27	27		F	F	F	F	
28	28		T	T	T	T	
29	29		F	F	F	F	
30	30		S	S	S	S	
31	31	CDR1	N	N	S	S	
32	32		Y	Y	Y	Y	
33	33		G	G	A	A	
34	34		M	M	V	M	
35	35		S	S	S	S	
36	36	FR2	W	W	W	W	
37	37		V	V	V	V	
38	38		R	R	R	R	
39	39		Q	Q	Q	Q	
40	40		N	A	A	A	Rare mouse, replace w/Hum
41	41		S	P	P	P	
42	42		D	G	G	G	Rare mouse, replace w/Hum
43	43		K	K	K	K	
44	44		R	G	G	G	
45	45		L	L	L	L	
46	46		E	E	E	E	
47	47		W	W	W	W	
48	48		V	V	V	V	
49	49		A	A	S	S	CDR contact/veneer
50	50	CDR2	S	S	A	A	
51	51		I	I	I	I	
52	52		R	R	S	S	
52A	53		S	S	G	G	
53	54		G	G	S	S	
54	55		G	G	G	G	

55	56		G	G	G	G
56	57		R	R	S	S
57	58		T	T	T	T
58	59		Y	Y	Y	Y
59	60		Y	Y	Y	Y
60	61		S	S	A	A
61	62		D	D	D	D
62	63		N	N	S	S
63	64		V	V	V	V
64	65		K	K	K	K
65	66		G	G	G	G
66	67	FR3	R	R	R	R
67	68		F	F	F	F
68	69		T	T	T	T
69	70		I	I	I	I
70	71		S	S	S	S
71	72		R	R	R	R
72	73		E	D	D	D
73	74		N	N	N	N
74	75		A	A	A	S
75	76		K	K	K	K
76	77		N	N	N	N
77	78		T	S	S	T
78	79		L	L	L	L
79	80		Y	Y	Y	Y
80	81		L	L	L	L
81	82		Q	Q	Q	Q
82	83		M	M	M	M
82A	84		S	N	N	N
82B	85		S	S	S	S
82C	86		L	L	L	L
83	87		K	R	R	R
84	88		S	A	A	A
85	89		E	E	E	E
86	90		D	D	D	D
87	91		T	T	T	T
88	92		A	A	A	A
89	93		L	L	L	V
90	94		Y	Y	Y	Y
91	95		Y	Y	Y	Y
92	96		C	C	C	C

93	97		V	V	A	A	Packing residue, use mouse
94	98		R	R	K	K	Canonical, use mouse
95	99	CDR3	Y	Y	D		
96	100		D	D	N		
97	101		H	H	Y		
98	102		Y	Y	D		
99	103		S	S	F		
100	104		G	G	W		
100A	105		S	S	S		
100B	106		S	S	G		
100C	107		-	-	T		
100D	108		-	-	F		
101	109		D	D	D		
102	110		Y	Y	Y		
103	111	FR4	W	W	W		
104	112		G	G	G		
105	113		Q	Q	Q		
106	114		G	G	G		
107	115		T	T	T		
108	116		T	L	L		
109	117		V	V	V		
110	118		T	T	T		
111	119		V	V	V		
112	120		S	S	S		
113	121		S	S	S		

Please replace the paragraph beginning at page 3, line 31 through page 4, line 4 with the following paragraph:

Figure 1 depicts an alignment of the amino acid sequences of the light chain of mouse 3D6 (amino acids 1-112 of SEQ ID NO:2), humanized 3D6 (amino acids 1-112 of SEQ ID NO:5), Kabat ID 109230 (amiono acids 1-112 of SEQ ID NO:6) and germline A19 antibodies (SEQ ID NO:7). CDR regions are indicated by arrows. Bold italics indicate rare murine residues. Bold indicates packing (VH + VL) residues. Solid fill indicates canonical/CDR interacting residues. Asterisks indicate residues selected for backmutation in humanized 3D6, version 1.

Please replace the paragraph beginning at page 4, line 5-7 with the following paragraph:

Figure 2 depicts an alignment of the amino acid sequences of the heavy chain of mouse 3D6 (amino acids 1-119 of SEQ ID NO:4), humanized 3D6 (amino acids 1-119 of SEQ ID NO:8), Kabat ID 045919 (SEQ ID NO:9) and germline VH3-23 antibodies (SEQ ID NO:10). Annotation is the same as for Figure 1.

Please replace the paragraph beginning at page 4, line 28-29 with the following paragraph:

Figure 9 depicts an alignment of the 10D5 VL (SEQ ID NO:14) and 3D6 VL (SEQ ID NO:2) amino acid sequences. Bold indicates residues that match 10D5 exactly.

Please replace the paragraph beginning at page 4, line 30-31 with the following paragraph:

Figure 10 depicts an alignment of the 10D5 VH (SEQ ID NO:16) and 3D6 VH (SEQ ID NO:4) amino acid sequences. Bold indicates residues that match 10D5 exactly.